

### **AMENDMENTS TO THE SPECIFICATION**

Please amend the specification as follows.

Delete Tables 1-9 and 11.

Delete paragraphs 0035-0082.

Add the following paragraphs after 0034.

The present invention relates to an isolated nucleic acid selected from the group consisting of (a) SEQ ID NO: 6527, (b) a DNA encoding the nucleic acid of (a), wherein the DNA is identical in length to (a); and (c) the complement of (a) or (b), wherein the complement is identical in length to the nucleic acid of (a) or (b). Additionally, the present invention relates to vectors or probes comprising a human insert, wherein the human insert consists of the nucleic acid selected from the group consisting of (a) SEQ ID NO: 6527, (b) a DNA encoding the nucleic acid of (a), wherein the DNA is identical in length to (a); and (c) the complement of (a) or (b), wherein the complement is identical in length to the nucleic acid of (a) or (b), and wherein the vector or probe comprises no other insert but the nucleic acid as described above.

The present invention also relates to an isolated nucleic acid selected from the group consisting of (a) SEQ ID NO: 15, (b) a DNA encoding the nucleic acid of (a), wherein the DNA is identical in length to (a); and (c) the complement of (a) or (b), wherein the complement is identical in length to the nucleic acid of (a) or (b). Additionally, the present invention relates to vectors or probes comprising a human insert, wherein the human insert consists of the nucleic acid selected from the group consisting of (a) SEQ ID NO: 15, (b) a DNA encoding the nucleic acid of (a), wherein the DNA is identical in length to (a); and (c) the complement of (a) or (b), wherein the complement is identical in length to the nucleic acid of (a) or (b), and wherein the vector or probe comprises no other insert but the nucleic acid as described above.

Delete paragraphs 0156-0161.

Add the following paragraphs and tables after paragraph 0155.

The nucleotide sequence of the predicted human GAM RNA (miRNA) GAM1032, which is described by Fig. 8, and its respective genomic source and genomic location are set forth in Tables 1-3. Table 1 describes the predicted human GAM RNA (miRNA) as set forth in SEQ ID NO: 15.

Table 1

GAM SEQ-ID	GAM NAME	GAM RNA SEQUENCE	GAM POS
=====	=====	=====	=====
15	GAM1032	CTAGACTGAAGCTCCTTGAGGA	A

Table 2 describes the GAM PRECURSOR RNA (hairpin) as set forth in SEQ ID NO: 6527 and how it relates to Fig. 8.

Table 2

GAM NAME	PRECUR SEQ-ID	PRECURSOR SEQUENCE	GAM DESCRIPTION
=====	=====	=====	=====
GAM1032	6527	GCTAGTCACT GGGGCAAAGA TGACTAAAAC ACTTTTCCTG CCCTCGAGGA GCTCACAGTC TAGTATGTCT CATCCCCTAC TAGACTGAAG CTCCTTGAGG ACAGGGATGG TCATACTCAC CTCGGTGTTG C	Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 1032 (GAM1032) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art GAM1032 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM1032 was detected is described with additional reference to Figs. 9-15 GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a human gene encoded by the human genome GAM1032 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1032 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1032 precursor RNA is designated SEQ ID:6527, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6527 is located from position 141427052 to position 141427182 relative to

chromosome 8 on the '-' strand. GAM1032 precursor RNA folds onto itself, forming GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional 'hairpin structure'. As is well known in the art, this 'hairpin structure', is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof. Nucleotide sequence of GAM1032 precursor RNA, designated SEQ ID NO: 6527, and a schematic representation of a predicted secondary folding of GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein. An enzyme complex designated DICER COMPLEX, 'dices' the GAM1032 folded precursor RNA yielding a GAM1032 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, 'dicing' of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1032 RNA, hereby incorporated herein. Expression of GAM1032 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs. 22 to 24. GAM1032 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1032 target RNA, herein designated GAM TARGET RNA. GAM1032 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5' untranslated region, a protein coding region and a 3' untranslated region, designated 5'UTR, PROTEIN CODING and 3'UTR respectively. GAM1032 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1032 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM1032 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3'UTR region, these target binding sites may be located instead in the 5'UTR region or in both 3'UTR and 5'UTR region. The complementary binding of GAM1032 RNA, herein designated GAM RNA, to target binding sites on GAM1032 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1032 target RNA into GAM1032 target protein, herein designated GAM TARGET PROTEIN, which is shown surrounded by a broken line. It is appreciated that GAM1032 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1032 target genes. The mRNA of each one of this plurality of GAM1032 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1032 RNA, herein designated GAM RNA, and which when bound by GAM1032 RNA causes inhibition of translation of the GAM1032 target mRNA into a corresponding GAM1032 target protein. The mechanism of the translational inhibition exerted by GAM1032 RNA, herein designated GAM RNA, on one or more GAM1032 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted by known miRNA genes. Nucleotide sequence of GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1032 folded precursor RNA, herein designated GAM FOLDED

PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein. Nucleotide sequences of a 'diced' GAM1032 RNA, herein designated GAM RNA, of GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1032 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1032 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein. It is appreciated that specific functions, and accordingly utilities, of GAM1032 RNA correlate with, and may be deduced from, the identity of the GAM1032 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

Table 3 shows data relating to the source and location of the GAM oligonucleotide, specifically the GAM PRECURSOR (hairpin) and its position in the human genome.

Table 3

GAM	PRECUR	ORGANISM	CHR	STR	CHR-START	CHR-END	SOURCE
NAME	SEQ-ID			AND	OFFSET	OFFSET	REF-ID
=====	=====	=====	=====	=====	=====	=====	=====
GAM	6527	hsa	8	-	141427052	141427182	
1032							

Table 4 shows a schematic representation of the GAM folded precursor as set forth in SEQ ID NO: 6527, beginning at the 5' end (beginning of upper row) to the 3' end (beginning of lower row), where the hairpin loop is positioned at the right part of the schematic.

Table 4

GAM	PREC	PRECURSOR	GAM FOLDED	PRECURSOR RNA
NAME	UR	-SEQUENCE		
		SEQ		
		-ID		

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=====
GAM   65  GCTAGTCACT   TAGT       CAAAG       AAACACTT       C       CA
1032  27  GGGGCAAAGA       TGT GC       CACTGGGG       ATGACTA       TTCCTG CCTCGAGGAGCT
      TGACTAAAAC   CAGTCTAGTA CG       GTGGCTCC       TACTGGT       AGGGAC GGAGTTCCTCGA
      ACTTTTCCTG   GTCAGATCAT   TT--       ACTCA       -----       A
      CCCTCGAGGA       A-       -- CTGATCCCC -----
      GCTCACAGTC
      TAGTATGTCT
      CATCCCTAC
      TAGACTGAAG
      CTCCTTGAGG
      ACAGGGATGG
      TCATACTCAC
      CTCGGTGTG
      C

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Table 5 shows the mature GAM RNA as set forth in SEQ ID NO: 15 as sliced by DICER from the GAM PRECURSOR sequence (hairpin) as set forth in SEQ ID NO: 6527.

Table 5

GAM NAME	GAM RNA SEQUENCE	PRECUR	SOURCE	GAM
		SEQ-ID	REF-ID	POS
=====	=====	=====	=====	=====
GAM1032	CTAGACTGAAGCTCCTTGAGGA	6527		A

Table 6 shows data relating to the SEQ ID NO of the GAM target binding site sequence of the target gene name as bound by the GAM RNA as set forth in SEQ ID NO: 15.

Table 6

TARGET	TARGET	TARGET BINDING SITE SEQUENCE
BINDING		
SITE		
SEQ-ID		
=====	=====	=====
3504	CHAT	TGCTCCTGCCACTAGGTTTCA
3505	CHAT	TGGGGAAGTGCGGTGACTGGGAAATGC
3506	CHAT	CCAGCGCACAGCCTGGGCAG
3507	CHAT	CATCCCTGCACCAGGACTCACCAAGA
3508	CHAT	CAAGACGCCCATCCTGGAAAAGGTCCC
3509	CHAT	AGGCAGCAGAGCCGAGGAGAGCAGGT
3510	CHAT	CGCGTCAGGCCAGCGCACAGCCTG

3511	CHAT	GCACAGCCTGGGCAGCTCAGCCTG
3512	CHAT	GAGCTAGGGGCAGGAGGCATG
3513	CHAT	GAGAAAGGAGTAGGAGCCTAGCA
3514	CHAT	GCCTCAAGGGGTGCGGCCCTCTCAG
3515	CHAT	GCGTCAGGCCAGCGCACAGCCTG
3516	CHAT	GCTCAGCCTGTCAGCTGAGCACGGGCG
3517	CHAT	GCTTTGAGAAAGGAGTAG
3518	CHAT	GGTGACTGGGAAATGCTGAG
3519	CHAT	GTCCGACCTCTGGAAATGT
3520	CHAT	GGCTCACACCCCCGCCACAC
3651	CTSK	GCACCCTAGAGGACTAGGGTA
3652	CTSK	CTTCCACGATGGTGCAGTG
3653	CTSK	CTTCCTACTTTGCTTCTCTCCA
3654	CTSK	CTTCCCTTCTTTGCAC
3655	CTSK	CTGACTTCTCACTTCCTAAG
3656	CTSK	CCTACTTTGCTTCTCTCCA
3657	CTSK	CCTTCCTACTTTGCTTCTCTC
3658	CTSK	GTCTATGTTTTCTACTCAA
3659	CTSK	GTACAGGTACAGGCTGGAGATT
3660	CTSK	CAGTGTAACGATGCACTTTGG
3661	CTSK	AATAAATCTAGCACCCCTGAT
3662	CTSK	TCTATTCATAAGTCTTTGGTACAAG
3663	CTSK	TCCTGCTCTTCCATTTCTTCC
3664	CTSK	TCCTACTTTGCTTCTCTCCA
3665	CTSK	TCCTCAAGGTAGAAATGTCTAT
3666	CTSK	TCCATCCTGCTCTTCCATTTCTTCCA
3667	CTSK	TGACTTCTCACTTCCTAAG
3668	CTSK	TCTTCCACGATGGTGCAGTG
3669	CTSK	TTGAAGCAGATGTGGTGA

3670	CTSK	TTGTCCCAGGGCTGATGCTGT
3671	CTSK	TTTCCAGCCGATCACTGGAGCT
4796	MPO	TTTATCCATAGACAGGGCCC
4797	MPO	TATTGAGCACCTACTACATGCA
4798	MPO	TCCTTGCCCTAGATGAGCCCAGC
4799	MPO	TCCTCACCCCTGATTTCTTGCTT
4800	MPO	TCAGGTGAGCTGTGGAGGTGGGGTC
4801	MPO	GGAGAAGAGAGATGGGGGTTCC
4802	MPO	GGAGCACAGCTCAGGAAGTAGA
4803	MPO	GGAGGTGGGGTCCTTGGAAGC
4804	MPO	GCTCCCCCTTTTTCTTCCTCA
4805	MPO	GCTCAGGAAGTAGACTGCCTG
4806	MPO	GCTGGGCTGTGTGGTTGACTT
4807	MPO	GCCCAGCCCTGTTCTGGGTGCAG
4808	MPO	GGGCCTGTTGCCCTTTCTGTACCA
4809	MPO	GGGAAGCCTCCTAAGGCCAGG
4810	MPO	GGCCAGGTAAGGGGGTGCAGCAGTGAG
4811	MPO	GGCTCCCCCTTTTTCTTCCTCACCT
4812	MPO	GGTGAGCTGTGGAGGTGGGG
4813	MPO	GAGCAAATTACCCTCCTTAAACAAGAG
4814	MPO	CTTGTAATTACATCTGTCATGGTTT
4815	MPO	CCTCAAGGAGGTCTGG
4816	MPO	CCTCTGGTTCTTCATTTATTGAG
4817	MPO	CTGAGTATGTGGAAGGCAGCA
4818	MPO	CTGAGTATGTGGAAGGCAGCAGCGGA
4819	MPO	AGGGCCCCTTGTATCCTCTG
4820	MPO	ATCTGTGTCCTGGTTAGCAGAGC
4821	MPO	CAGCTCAGGAAGTAGACTGCCT
4822	MPO	CCCTCAAGGAGGTCTGG



4823	MPO	ACAGCTCAGGAAC TAGACTGCCT
4824	MPO	AGGCAGCAGAGCGGACTGGTGA
4825	MPO	AAGGCAGCAGAGCGGACTGGTGA
5322	SERPIN	TGAAGCTCTCACACGCACAG
5323	SERPIN	CAGTCTGGAGGGTCCTGGCC
5324	SERPIN	CATGTGTGGCCCTGTCTGCTTA
5325	SERPIN	CCCATGGACTCTTCAGTCTGG
5326	SERPIN	ATGTGTGGCCCTGTCTGCTTA
5327	SERPIN	AGTAGGAACTTGGAATGCAAG
5328	SERPIN	GAAGCTCTCACACGCACAG
5329	SERPIN	CCTGTGCACCGTAGTGGCCATGG
5330	SERPIN	CTCTTCAGTCTGGAGGGTCCTGG
5331	SERPIN	GCCCATGGACTCTTCAGTCTGG
5541	TNFRSF	GTGAAAAACAACAAATTCAGTTCTGA
5542	TNFRSF	GTGACACACAGGTGTTCAAAGACG
5543	TNFRSF	GGCAAGACTGCCCTTAGAAATTCTAG
5544	TNFRSF	GCGTATGACACATTGA
5545	TNFRSF	GCCAGCCCTGGCTGCCCAGGCGGAG
5546	TNFRSF	GACGCTTCTGGGGAGTGAGGGAA
5547	TNFRSF	GACAATGTCCAAGACACAGCAGA
5548	TNFRSF	CTTTGCCACCTCTCCATTTTGGC
5549	TNFRSF	CTGCCCTTAGAAATTCTAGCC
5550	TNFRSF	CTGGCTCAAACTACCTA
5551	TNFRSF	CGCAAGAGTGACACACAGGTGTTCA
5552	TNFRSF	ATGTCCAAGACACAGCAGAACAGA
5553	TNFRSF	ATGCAGAAAGCACAGAAAGGA
5554	TNFRSF	ATGTAACTGTGAAGATAGTT
5555	TNFRSF	ATGGAAAGAAAGAAGCGTATGACACA
5556	TNFRSF	ATGGAAAGAAAGAAGCGTATGACACAT

5557 TNFRSF ATTTAAATAAGGCTCTACCTC  
 5558 TNFRSF ACAATGTCCAAGACACAGCAGA  
 5559 TNFRSF TCCTCAAGGACATTACTAG  
 5560 TNFRSF TCTCAGGCATCAAAAGCATTTTG  
 5561 TNFRSF TCCAAGGATGTTTAAATCTAGTTGG  
 5562 TNFRSF TGGGTGAAGAGAAAGGAAGTACAGA  
 5563 TNFRSF TCTTTCTCAGGCATCAAAAGCATT  
 5564 TNFRSF TTGGGTGAAGAGAAAGGAAGTACAGA

Table 7, lines 1468-1501 shows data relating to target genes and binding site of GAM oligonucleotides.

Table 7

GAM NAME	GAM RNA SEQUENCE	TARGET	TAR GET	UTR	TARGET BS-SEQ	BINDING-SITE	DRAW	GAM
			REF-ID			(UPPER:GAM; LOWER:TARGET)		POS
=====	=====	=====	=====	==	=====	=====		=====
GAM103 2	CTAGACTG AAG CTCCTTGA GGA	CHAT	NM_02 0984. 1	5	GCCTCA AGGGGT G CGGCC TCTCAG	- --- AA CT AGA CTG GA TCT GGC C CCC G-	A GCTCCTTGAGG TGGGGAAGTCC G	A
GAM103 2	CTAGACTG AAG CTCCTTGA GGA	CTSK	NM_00 0396. 2	3	TCCTCA AGGTAG A AATGTC TAT	C TGAAG - TAGAC CT CCTTGAGGA ATCTG GA GGAAGTCTCT T TAAA- T	A TAGAC ATCTG T	A
GAM103 2	CTAGACTG AAG CTCCTTGA GGA	MPO	NM_00 0250. 1	5	CCCTCA AGGAGG T CTGG	TGAAG CTAGAC GGTCTG -----	A CTCCTTGAGG GAGGAAGTCC C	A
GAM103 2	CTAGACTG AAG CTCCTTGA GGA	MPO	NM_00 0250. 1	5	CCTCAA GGAGGT C TGG	TGAAG CTAGAC CTCCTTGAGG GGTCTG GAGGAAGTCC -----	A TAGAC GGTCTG	A
GAM103 2	CTAGACTG AAG CTCCTTGA	SERPI NA	NM_00 1085. 2	3	CCCATG GACTCT T	C- T A CTAGACTGAAG TCC TG GG GGTCTGACTTC AGG AC CC	A TCC TG GG AGG AC CC	A

	GGA				CAGTCT		TC	T	-	
					GG					
GAM103	CTAGACTG	SERPI	NM_00	3	GCCCAT		C-	T	A	A
2	AAG	NA 3	1085.		GGACTC	CTAGACTGAAG	TCC	TG	GG	
	CTCCTTGA		2		T	GGTCTGACTTC	AGG	AC	CC	
	GGA				TCAGTC		TC	T	-	G
					TGG					
GAM103	CTAGACTG	TNFRS	NM_15	3	TCCTCA	AC	AGC	CTAG	TGA	A
2	AAG	F6	2874.		AGGACA	TCCTTGAGGA	GATC	ATT		
	CTCCTTGA		1		T	AGGAACTCCT	--	AC-		
	GGA				TACTAG					

It is appreciated that the specific functions and accordingly the utilities a GAM oligonucleotide that is described by Fig. 8 is correlated with and may be deduced from the identity of the GAM TARGET GENES inhibited thereby, and whose functions are set forth in Table 8. Table 8 shows data relating to the function and utilities of GAM RNA as set forth in SEQ ID NO: 15.

Table 8

GAM	TARGET	GAM RNA	GAM FUNCTION	GAM TAR
NAME		SEQUENCE		POS DIS
=====	=====	=====	=====	====

GAM1	TNFRSF	CTAGACTG	TNFRSF6 (Accession	A	A
032	6	AAGCTCC	NM_152874.1) is another		
		TTGAGGA	GAM1032 target gene. TNFRSF6		
			BINDING SITE is a target		
			binding site found in the 3`		
			untranslated region of		
			multiple transcripts of mRNA		
			encoded by TNFRSF6,		
			corresponding to a target		
			binding site such as BINDING		
			SITE I, BINDING SITE II or		
			BINDING SITE III of Fig.8.		
			Nucleotide sequences of		
			TNFRSF6 BINDING SITE, and		
			secondary structure		
			complementarity to the		
			nucleotide sequence of		
			GAM1032 RNA are set forth in		
			Tables 6 and 7, hereby		
			incorporated herein.		
			Another function		
			of GAM1032 is therefore		
			inhibition of TNFRSF6.		
			Accordingly, utilities of		
			GAM1032 include diagnosis,		
			prevention and treatment of		
			Alzheimer, and of other		
			diseases and clinical		
			conditions associated with		
			TNFRSF6.		

GAM	CHAT	CTAGACTG	Choline Acetyltransferase	A	A
1032		AAGCTCC	(CHAT, Accession		
		TTGAGGA	NM_020984.1) is a GAM1032		
			target gene. CHAT BINDING		
			SITE is a target binding		
			site found in the 5`		
			untranslated region of		
			multiple transcripts of mRNA		
			encoded by CHAT,		
			corresponding to a target		
			binding site such as BINDING		
			SITE I, BINDING SITE II or		
			BINDING SITE III of Fig.8.		
			Nucleotide sequences of CHAT		
			BINDING SITE, and secondary		
			structure complementarity to		
			the nucleotide sequence of		
			GAM1032 RNA are set forth in		
			Tables 6 and 7, hereby		
			incorporated herein. A		
			function of GAM1032 is		
			therefore inhibition of		

CHAT, a GAM1032 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT. The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1	CTSK	CTAGACTG	CTSK (Accession	A	A
032		AAGCTCC	NM_000396.2) is another		
		TTGAGGA	GAM1032 target gene. CTSK		
			BINDING SITE is a target		
			binding site found in the 3`		
			untranslated region of mRNA		
			encoded by CTSK,		
			corresponding to a target		
			binding site such as BINDING		
			SITE I, BINDING SITE II or		
			BINDING SITE III of Fig.8.		
			Nucleotide sequences of CTSK		
			BINDING SITE, and secondary		
			structure complementarity to		
			the nucleotide sequence of		
			GAM1032 RNA are set forth in		
			Tables 6 and 7, hereby		
			incorporated herein.		

Another function of GAM1032 is therefore inhibition of CTSK. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM1	MPO	CTAGACTG	Myeloperoxidase (MPO,	A	A
032		AAGCTCC	Accession NM_000250.1) is		
		TTGAGGA	another GAM1032 target gene.		
			MPO BINDING SITE1 and MPO		
			BINDING SITE2 are target		
			binding sites found in		

untranslated regions of mRNA encoded by MPO, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE1 and MPO BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein. Another function of GAM1032 is therefore inhibition of MPO, a GAM1032 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO. The function of MPO has been established by previous studies. Weil et al. (1988) found that the MPO gene was translocated to chromosome 15 in all cases of acute promyelocytic leukemia (subtype M3), which is consistently associated with the chromosomal translocation t(15;17)(q22;q11.2). In 2 of 4 cases examined by genomic blot analysis, rearrangement of the MPO gene was detected in leukemia cells. Weil et al. (1988) also suggested that MPO may be pivotal in the pathogenesis of APL. According to HGM10, the MPO gene is located at a distance from the breakpoint in APL, and the gene itself is probably usually not rearranged in APL. Myeloperoxidase has been detected in activated microglial macrophages and

within amyloid plaques in the central nervous system. Using statistical analysis, Reynolds et al. (2000) examined the relationship between APOE (OMIM Ref. No. 107741) and MPO polymorphisms in the risk of Alzheimer disease (AD; 104300) in a genetically homogeneous Finnish population. They found that the presence of the MPO A allele in conjunction with APOE E4 significantly increased the risk of AD in men, but not in women (odds ratio for men with both alleles = 11.4 vs APOE E4 alone = 3.0). Reynolds et al. (2000) also found that estrogen receptor- alpha (OMIM Ref. No. 133430) binds to the MPO A promoter, which may explain the gender differences. Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference: Reynolds, W. F.; Hiltunen, M.; Pirskanen, M.; Mannermaa, A.; Helisalmi, S.; Lehtovirta, M.; Alafuzoff, I.; Soininen, H. : MPO and APOE epsilon- 4 polymorphisms interact to increase risk for AD in Finnish males. *Neurology* 55: 1284- 1290, 2000. ; and Weil, S. C.; Rosner, G. L.; Reid, M. S.; Chisholm, R. L.; Lemons, R. S.; Swanson, M. S.; Carrino, J. J.; Diaz, M. O.; Le Beau, M. M. : Translocation and rearrangement of myeloperoxidase. Further studies establishing the function and utilities of MPO are found in John Hopkins OMIM database record ID 606989, and in cited publications listed in Table 9, hereby incorporated

herein.

GAM1	SERPIN	CTAGACTG	Serine (or cysteine)	A	A
032	A 3	AAGCTCC	Proteinase Inhibitor, Clade		
		TTGAGGA	A (alpha- 1 antiprotei		

(SERPINA3, Accession NM\_001085.2) is another GAM1032 target gene. SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINA3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1032 is therefore inhibition of SERPINA3, a GAM1032 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3. The function of SERPINA3 has been established by previous studies. Alpha- 1- antichymotrypsin is a plasma protease inhibitor synthesized in the

liver. It is a single glycopeptide chain of about 68,000 daltons and belongs to the class of serine protease inhibitors. In man, the normal serum level is about one- tenth that of alpha- 1- antitrypsin (PI; 107400), with which it



shares nucleic acid and protein sequence homology (Chandra et al. 1983). Both are major acute phase reactants; their concentrations in plasma increase in response to trauma, surgery, and infection. Antithrombin III, which also is structurally similar to alpha-1-antitrypsin, shows less sequence homology to antichymotrypsin and is not an acute phase reactant. Kelsey et al. (1988) cloned and analyzed the AACT gene, partly because of the possibility that genetic variation in other protease inhibitors may influence the prognosis in AAT deficiency. They isolated the AACT gene on a series of cosmid clones, with restriction mapping of about 70 kb around the gene. Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Chandra, T.; Stackhouse, R.; Kidd, V. J.; Robson, K. J. H.; Woo, S. L. C. : Sequence homology between human alpha-1-antichymotrypsin, alpha-1-antitrypsin, and antithrombin III. Biochemistry 22: 5055- 5061, 1983. ; an Kelsey, G. D.; Abeliovich, D.; McMahon, C. J.; Whitehouse, D.; Corney, G.; Povey, S.; Hopkinson, D. A.; Wolfe, J.; Mieli-Vergani, G.; Mowat, A. P. : Cloning of the human alpha-1 antichym Further studies establishing the function and utilities of SERPINA3 are found in John Hopkins OMIM database record ID 107280, and in cited publications listed in Table

9, hereby incorporated  
herein.

Studies documenting the well known correlations between GAM TARGET GENES that are described by Fig.8 and the known gene functions and related diseases are listed in Table 9. Specifically, Table 9 describes references of GAM target genes, as set forth in SEQ ID NO:15 in Table 8.

Table 9

GAM	GAM RNA	TARGET	REFERENCES	GAM
NAME	SEQUENCE			POS
=====	=====	=====	=====	=====
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	CHAT	Barrard, B. A.; Lottspeich, F.; Braun, A.; Barde, Y. A.; Mallet, J.: cDNA cloning and complete sequence of porcine choline acetyltransferase: in vitro translation of the corresponding RNA yields an active protein. Proc.Nat. Acad. Sci. 84:9280 - 9284, 1987.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	CHAT	Chireux, M. A.; Le Van Thai, A.; Weber, M. J.: Human choline acetyltransferase gene: localization of alternative first exons. J. Neurosci. Res. 40:427 - 438, 1995.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	CHAT	Cohen - Haguenauer, O.; Brice, A.; Berrard, S.; Van Cong, N.; Mallet, J.; Frezal, J.: Localization of the choline acetyltransferase (CHAT) gene to human chromosome 10. Genomics 6: 374-378, 1990.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	CHAT	Erickson, J. D.; Varoqui, H.; Schafer, M. K. - H.; Modi, W.; Diebler, M. - F.; Weihe, E.; Rand, J.; Eiden, L. E.; Bonner, T. I.; Usdin, T.B.: Functional identification of a vesicular acetylcholine transporter and its expression from a 'cholinergic' gene locus. J. Biol. Chem. 269:21929 - 21932, 1994.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	CHAT	Misawa, H.; Ishii, K.; Deguchi, T.: Gene expression of mouse choline acetyltransferase: alternative splicing and identification of a highly active promoter region. J. Biol. Chem. 267:	A

20392 - 20399, 1992.

GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	CHAT	Ohno, K.; Tsujino, A.; Brengman, J. M.; Harper, C. M.; Bajzer, Z.; Udd, B.; Beyring, R.; Robb, S.; Kirkham, F. J.; Engel, A. G.: Choline acetyltransferase mutations cause myasthenic syndrome associated with episodic apnea in humans. Proc. Nat. Acad. Sci. 98: 2017 - 2022, 2001.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	CHAT	Strauss, W. L.; Kemper, R. R.; Jayakar, P.; Kong, C. F.; Hersh, L. B.; Hilt, D. C.; Rabin, M.: Human choline acetyltransferase gene maps to region 10q11 - q22.2 by in situ hybridization. Genomics 9:396 - 398, 1991.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	CHAT	Toussaint, J. L.; Geoffroy, V.; Schmitt, M.; Werner, A.; Garnier, J. M.; Simoni, P.; Kempf, J.: Human choline acetyltransferase (CHAT): partial gene sequence and potential control regions. Genomics 12:412 - 416, 1992.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	CHAT	Viegas - Pequignot, E.; Berrard, S.; Brice, A.; Apiou, F.; Mallet, J.: Localization of a 900 - bp - long fragment of the human choline acetyltransferase gene to 10q11.2 by nonradioactive in situ hybridization. Genomics 9:210 - 212, 1991.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Borregaard, N.; Cowland, J. B.: Granules of the human neutrophilic polymorphonuclear leukocyte. Blood 89: 3503 - 3521, 1997.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Chang, K. S.; Schroeder, W.; Siciliano, M. J.; Thompson, L. H.; McCredie, K.; Beran, M.; Freireich, E. J.; Liang, J. C.; Trujillo, J. M.; Stass, S. A.: The localization of the human myeloperoxidase gene is in close proximity to the translocation breakpoint in acute promyelocytic leukemia. Leukemia 1: 458 - 462, 1987.	A
GAM103 2	CTAGAC TGAAGC TC	MPO	DeLeo, F. R.; Goedken, M.; McCormick, S. J.; Nauseef, W. M.: A novel form of hereditary	A

	CTTGAG GA		myeloperoxidase deficiency linked to endoplasmicreticulum/proteasome degradation. J. Clin. Invest. 101: 2900 - 2909,1998.	
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Eiserich, J. P.; Baldus, S.; Brennan, M. - L.; Ma, W.; Zhang, C.;Tousson, A.; Castro, L.; Lysis, A. J.; Nauseef, W. M.; White, C. R.;Freeman, B. A.: Myeloperoxidase, a leukocyte - derived vascular NOoxidase. Science 296: 2391 - 2394, 2002.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Inazawa, J.; Inoue, K.; Nishigaki, H.; Tsuda, S.; Taniwaki, M.;Misawa, S.; Abe, T.: Assignment of the human myeloperoxidase gene(MPO) to bands q21.3 - q23 of chromosome 17. Cytogenet. Cell Genet. 50:135 - 136, 1989.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Johnson, K.; Gemperlein, I.; Hudson, S.; Shane, S.; Rovera, G.: Complete nucleotide sequence of the human myeloperoxidase gene. NucleicAcids Res. 17: 7985 - 7986, 1989.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Kizaki, M.; Miller, C. W.; Selsted, M. E.; Koeffler, H. P.: Myeloperoxidase(MPO) gene mutation in hereditary MPO deficiency. Blood 83: 1935 - 1940,1994.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Klebanoff, S. J.: Myeloperoxidase. Proc. Assoc. Am. Physicians 111:383 - 389, 1999.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Kudoh, J.; Minoshima, S.; Hashinaka, K.; Nishio, C.; Yamada, M.;Shimizu, Y.; Shimizu, N.: Assignment of the myeloperoxidase (MPO)gene to human chromosome 17. (Abstract) Cytogenet. Cell Genet. 46:641 - 642, 1987.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Kudoh, J.; Minoshima, S.; Hashinaka, K.; Nishio, C.; Yamada, M.;Shimizu, Y.; Shimizu, N.: Assignment of the myeloperoxidase geneMPO to human chromosome 17 using somatic cell hybrids and flow - sortedchromosomes. Jpn. J. Hum. Genet. 33: 315 - 324, 1988.	A

GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Law, D. J.; Prasad, M. A.; King, S. E.; Spranger, K. D.; Lee, Y. H.; Fox, R. E.; Collins, E. E.; Gebuhr, T. C.; Miller, D. E.; Petty, E. M.: Localization of the human estrogen - responsive finger protein(EFP) gene (ZNF147) within a YAC contig containing the myeloperoxidase(MPO) gene. Genomics 28: 361 - 363, 1995.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Le Beau, M. M.; Lemons, R. S.; Rosner, G. L.; Carrino, J. C.; Reid, M. S.; Chisholm, R. L.; Diaz, M. O.; Weil, S. C.: Chromosomal localization of the gene encoding myeloperoxidase. (Abstract) Cytogenet. Cell Genet. 46: 645, 1987.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Liang, J. C.; Chang, K. S.; Schroeder, W. T.; Freireich, E. J.; Stass, S. A.; Trujillo, J. M.: The myeloperoxidase gene is translocated from chromosome 17 to 15 in a patient with acute promyelocytic leukemia. Cancer Genet. Cytogenet. 30: 103 - 107, 1988.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Liang, J. C.; Chang, K. S.; Schroeder, W.; Siciliano, M.; Trujillo, J.; Stass, S.: The human myeloperoxidase gene locates on chromosome 17q22 - 24 and is translocated in acute promyelocytic leukemia. (Abstract) Am. J. Hum. Genet. 41: A226, 1987.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Miki, T.; Weil, S. C.; Rosner, G. L.; Reid, M. S.; Kidd, K. K.: An MPO cDNA clone identifies an RFLP with PstI. Nucleic Acids Res. 16:1649, 1988.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Morishita, K.; Kubota, N.; Asano, S.; Kaziyo, Y.; Nagata, S.: Molecular cloning and characterization of cDNA for human myeloperoxidase. J. Biol. Chem. 262: 3844 - 3851, 1987.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Murao, S. - I.; Stevens, F. J.; Ito, A.; Huberman, E.: Myeloperoxidase: a myeloid cell nuclear antigen with DNA - binding properties. Proc. Nat. Acad. Sci. 85: 1232 - 1236, 1988.	A
GAM103 2	CTAGAC TGAAGC TC	MPO	Nauseef, W. M.; Brigham, S.; Cogley, M.: Hereditary myeloperoxidase deficiency due to a	A

	CTTGAG GA		missense mutation of arginine 569 to tryptophan. J.Biol. Chem. 269: 1212 - 1216, 1994.	
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Nauseef, W. M.; Olsson, I.; Arnljots, K.: Biosynthesis and processing of myeloperoxidase - a marker for myeloid cell differentiation. Europ.J. Haemat. 40: 97 - 110, 1988.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Nauseef, W.; Cogley, M.; McCormick, S.: Effect of the R569W missense mutation on the biosynthesis of myeloperoxidase. J. Biol. Chem. 271:9546 - 9549, 1996.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Reynolds, W. F.; Hiltunen, M.; Pirskanen, M.; Mannermaa, A.; Helisalmi, S.; Lehtovirta, M.; Alafuzoff, I.; Soininen, H.: MPO and APOE epsilon - 4 polymorphisms interact to increase risk for AD in Finnish males. Neurology 55:1284 - 1290, 2000.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Robinson, T. J.; Morris, D. J.; Ledbetter, D. H.: Chromosomal assignment and regional localization of myeloperoxidase in the mouse. Cytogenet. Cell Genet. 53: 83 - 86, 1990.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Romano, M.; Dri, P.; Dadalt, L.; Patriarca, P.; Baralle, F. E.: Biochemical and molecular characterization of hereditary myeloproliferative deficiency. Blood 90: 4126 - 4134, 1997.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	van Tuinen, P.; Johnson, K. R.; Ledbetter, S. A.; Nussbaum, R.L.; Rovera, G.; Ledbetter, D. H.: Localization of myeloperoxidase to the long arm of human chromosome 17: relationship to the 15;17 translocation of acute promyelocytic leukemia. Oncogene 1: 319 - 322, 1987.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Weil, S. C.; Rosner, G. L.; Reid, M. S.; Chisholm, R. L.; Farber, N. M.; Spitznagel, J. K.; Swanson, M. S.: cDNA cloning of human myeloperoxidase: decrease in myeloperoxidase mRNA upon induction of HL - 60 cells. Proc. Nat. Acad.	A

Sci. 84: 2057 - 2061, 1987.

GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Weil, S. C.; Rosner, G. L.; Reid, M. S.; Chisholm, R. L.; Lemons, R. S.; Swanson, M. S.; Carrino, J. J.; Diaz, M. O.; Le Beau, M. M.: Translocation and rearrangement of myeloperoxidase gene in acute promyelocytic leukemia. Science 240: 790 - 792, 1988.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Yamada, M.; Hur, S. - J.; Hashinaka, K.; Tsuneoka, K.; Saeki, T.; Nishio, C.; Sakiyama, F.; Tsunasawa, S.: Isolation and characterization of a cDNA coding for human myeloperoxidase. Arch. Biochem. Biophys. 255:147 - 155, 1987.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	MPO	Zaki, S. R.; Austin, G. E.; Chan, W. C.; Conaty, A. L.; Trusler, S.; Trappier, S.; Lindsey, R. B.; Swan, D. C.: Chromosomal localization of the human myeloperoxidase gene by in situ hybridization using oligonucleotide probes. Genes Chromosomes Cancer 2: 266 - 270, 1990.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Chandra, T.; Stackhouse, R.; Kidd, V. J.; Robson, K. J. H.; Woo, S. L. C.: Sequence homology between human alpha - 1 - antichymotrypsin, alpha - 1 - antitrypsin, and antithrombin III. Biochemistry 22: 5055 - 5061, 1983.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Eriksson, S.; Lindmark, B.; Lilia, H.: Familial alpha - 1 - antichymotrypsin deficiency. Acta Med. Scand. 220: 447 - 453, 1986.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Gilfix, B. M.; Briones, L.: Absence of the A1252G mutation in alpha 1 - antichymotrypsin in a North American population suffering from dementia. J. Cereb. Blood Flow Metab. 17: 233 - 235, 1997.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Haines, J. L.; Pritchard, M. L.; Saunders, A. M.; Schildkraut, J. M.; Growdon, J. H.; Gaskell, P. C.; Farrer, L. A.; Auerbach, S. A.; Gusella, J. F.; Locke, P. A.; Rosi, B. L.; Yamaoka, L.; Small, G. W.; Conneally, P. M.; Roses, A. D.;	A

			Pericak - Vance, M. A.: No geneticeffect of alpha - 1 - antichymotrypsin in Alzheimer disease. Genomics 33:53 - 56, 1996.	
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Haines, J. L.; Scott, W. K.; Pericak - Vance, M. A.: Reply to 'Geneticeffect of alpha - 1 - antichymotrypsin on the risk of Alzheimer disease.' (Letter) Genomics 40: 384 - 385, 1997.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Kamboh, M. I.; Aston, C. E.; Ferrell, R. E.; Dekosky, S. T.: Geneticeffect of alpha - 1 - antichymotrypsin on the risk of Alzheimer disease. (Letter) Genomics 41: 382 - 385, 1997.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Kamboh, M. I.; Sanghera, D. K.; Ferrell, R. E.; DeKosky, S. T.: APOE*4 - associated Alzheimer's disease risk is modified by alpha - 1 - antichymotrypsinpolymorphism. Nature Genet. 10: 486 - 488, 1995.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Kelsey, G. D.; Abeliovich, D.; McMahon, C. J.; Whitehouse, D.; Corney, G.; Povey, S.; Hopkinson, D. A.; Wolfe, J.; Mieli - Vergani, G.; Mowat, A. P.: Cloning of the human alpha - 1 antichymotrypsin geneand genetic analysis of the gene in relation to alpha - 1 antitrypsindeficiency. J. Med. Genet. 25: 361 - 368, 1988.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Morgan, K.; Licastro, F.; Tilley, L.; Ritchie, A.; Morgan, L.; Pedrini, S.; Kalsheker, N.: Polymorphism in the alpha - 1 - antichymotrypsin(ACT) gene promoter: effect on expression in transfected glial andliver cell lines and plasma ACT concentrations. Hum. Genet. 109:303 - 310, 2001.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Morgan, K.; Morgan, L.; Carpenter, K.; Lowe, J.; Lam, L.; Cave, S.; Xuereb, J.; Wischik, C.; Harrington, C.; Kalsheker, N. A.: Microsatellitepolymorphism of the alpha - 1 - antichymotrypsin gene locus associatedwith sporadic Alzheimer's disease. Hum. Genet. 99: 27 - 31, 1997.	A



GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Munoz, E.; Obach, V.; Oliva, R.; Marti, M. J.; Ezquerro, M.; Pastor, P.; Ballesta, F.; Tolosa, E.: Alpha - 1 - antichymotrypsin gene polymorphism and susceptibility to Parkinson's disease. Neurology 52: 297 - 301, 1999.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Poller, W.; Faber, J. - P.; Scholz, S.; Weidinger, S.; Bartholome, K.; Olek, K.; Eriksson, S.: Mis - sense mutation of alpha - 1 - antichymotrypsin gene associated with chronic lung disease. (Letter) Lancet 339:1538, 1992.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Poller, W.; Faber, J. - P.; Weidinger, S.; Tief, K.; Scholz, S.; Fischer, M.; Olek, K.; Kirchgesser, M.; Heidtmann, H. - H.: A leucine - to - proline substitution causes a defective alpha - 1 - antichymotrypsin allele associated with familial obstructive lung disease. Genomics 17: 740 - 743, 1993.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Rabin, M.; Watson, M.; Breg, W. R.; Kidd, V.; Woo, S. L. C.; Ruddle, F. H.: Human alpha - 1 - antichymotrypsin and alpha - 1 - antitrypsin (PI) genes map to the same region on chromosome 14. (Abstract) Cytogenet. Cell Genet. 40: 728, 1985.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Rabin, M.; Watson, M.; Kidd, V.; Woo, S. L. C.; Breg, W. R.; Ruddle, F. H.: Regional location of alpha - 1 - antichymotrypsin and alpha - 1 - antitrypsin genes on human chromosome 14. Somat. Cell Molec. Genet. 12: 209 - 214, 1986.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Samilchuk, E. I.; Chuchalin, A. G.: Mis - sense mutation of alpha - 1 - antichymotrypsin gene and chronic lung disease. (Letter) Lancet 342: 624, 1993.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Sefton, L.; Kearney, P.; Kelsey, G.; Povey, S.; Wolfe, J.: Physical linkage of the genes PI and AACT. (Abstract) Cytogenet. Cell Genet. 51:1076, 1989.	A

GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Sefton, L.; Kelsey, G.; Kearney, P.; Povey, S.; Wolfe, J.: Aphysical map of the human PI and AACT genes. Genomics 7: 382 - 388,1990.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Tachikawa, H.; Tsuda, M.; Onoe, K.; Ueno, M.; Takagi, S.; Shinohara, Y.: Alpha - 1 - antichymotrypsin gene A1252G variant (ACT Isehara - 1) is associated with a lacunar type of ischemic cerebrovascular disease. J.Hum. Genet. 46: 45 - 47, 2001.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Tsuda, M.; Sei, Y.; Matsumoto, M.; Kamiguchi, H.; Yamamoto, M.; Shinohara, Y.; Igarashi, T.; Yamamura, M.: Alpha - 1 - antichymotrypsinvariant detected by PCR - single strand conformation polymorphism (PCR - SSCP) and direct sequencing. Hum. Genet. 90: 467 - 468, 1992.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Tsuda, M.; Sei, Y.; Yamamura, M.; Yamamoto, M.; Shinohara, Y.: Detection of a new mutant alpha - 1 - antichymotrypsin in patients with occlusive - cerebrovascular disease. FEBS Lett. 304: 66 - 68, 1992.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Wang, X.; DeKosky, S. T.; Luedeking - Zimmer, E.; Ganguli, M.; Kamboh, M. I.: Genetic variation in alpha - 1 - antichymotrypsin and its association with Alzheimer's disease. Hum. Genet. 110: 356 - 365, 2002.	A
GAM103 2	CTAGAC TGAAGC TC CTTGAG GA	SERPIN A3	Yamamoto, M.; Kondo, I.; Ogawa, N.; Asanuma, M.; Yamashita, Y.; Mizuno, Y.: Genetic association between susceptibility to Parkinson's disease and alpha - 1 - antichymotrypsin polymorphism. Brain Res. 759:153 - 155, 1997.	A

Table 11 shows data relating to Alzheimer's and ALL diseases for which GAM RNA SEQ ID NO: 15 is predicted to regulate the disease-associated genes.

Table 11

ROW	DISEASE	TARGET-GENES	ASSOCIATED WITH ALZHEIMER DISEASE
#	NAME		
=====	=====	=====	=====

- 1 ALL PLAU, CNTF, AVP, CRYAB, SNCB, APBA2, DHCR24, CTNND2, PSEN1, APLP1, GSK3B, APPBP2, DSCR1, MME, CRAT, AGER, NCSTN, ABCD1, BCHE, A2M, MTNR1A, APOC1, THOP1, APBA1, SERPINA3, ACHE, UBB, PIN1, TNFSF5, ADAM17, BACE2, PLCD1, APLP2, CTSK, BACE, SOD2, ADAM10, DLST, CTSG, NPY, OGDH, GYPA, PRND, CHAT, PSEN2, ACE, RAGE, GAL, APBB1, TRPM2, GSN, SNCA, BLMH, IL1A, TNFRSF6, HADH2, FHL2, ARHA, MAPK10, SLC6A4, OLR1, TGFB1, FLNB, TNF, ADAMTS5, SNCAIP, SNCG, MAPT, TFCP2, TNFRSF5, IAPP, CLU, B2M, VLDLR, GLUL, CAV2, IDE, NCKAP1, APBB2, FOS, ESR2, ACT, NGB, FPRL1, HTR2C, APCS, IGF1, CASP3, IL1B, HTR2A, GFAP, CRH, APP, SLC17A7, LRP1, PRNP, MPO, NOTCH1, S100B, MT3, CAV1, HD, BAX and CTSB.
- 2 Alzhei AVP, NCSTN, ARHA, APPBP2, HTR2A, PSEN1, DHCR24, mer PLAU, MTNR1A, SERPINA3, DSCR1, APBA1, APOC1, BCHE, MME, BACE2, UBB, CTNND2, APLP1, APP, SLC17A7, NCKAP1, GFAP, IGF1, SLC6A4, HD, S100B, CASP3, MPO, CNTF, GSK3B, CRH, LRP1, MT3, APBA2, CAV1, CRYAB, MAPK10, TGFB1, CHAT, TNFRSF5, CTSB, MAPT, OLR1, FLNB, CAV2, GLUL, IAPP, NGB, ACT, FOS, APBB2, TNF, SNCAIP, APLP2, PSEN2, OGDH, GYPA, ADAM17, ADAM10, ADAMTS5, BACE, TNFRSF6, ACE, HTR2C, RAGE, HADH2, FHL2, PRND, IL1A, SNCA, DLST, CTSK, TRPM2, BLMH.